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## SEQUENCE LISTING

<110> TUMER, NILGUN E.  
WANG, PINGER

<120> TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN

<130> OCIRS 3.3-060 CONT

<140> 09/721,047

<141> 2000-11-22

<160> 19

<170> PatentIn Ver. 2.1

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<212> DNA

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ggggggagtga aacctcagct gctaaaaaaa cgttgtaaga aaaaaagaaa gttgtgagtt 180
aactacaggg cgaaagtatt ggaactagct agtaggaagg gaag atg aag tcg atg 236
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ctt gtg gtg aca ata tca ata tgg ctc att ctt gca cca act tca act 284
Leu Val Val Thr Ile Ser Ile Trp Leu Ile Leu Ala Pro Thr Ser Thr
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tgg gct gtg aat aca atc atc tac aat gtt gga agt acc acc att agc 332
Trp Ala Val Asn Thr Ile Ile Tyr Asn Val Gly Ser Thr Thr Ile Ser
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aaa tac gcc act ttt ctg aat gat ctt cgt aat gaa gcg aaa gat cca 380
Lys Tyr Ala Thr Phe Leu Asn Asp Leu Arg Asn Glu Ala Lys Asp Pro
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agt tta aaa tgc tat gga ata cca atg ctg ccc aat aca aat aca aat 428
Ser Leu Lys Cys Tyr Gly Ile Pro Met Leu Pro Asn Thr Asn Thr Asn
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cca aag tac gtg ttg gtt gag ctc caa ggt tca aat aaa aaa acc atc 476
Pro Lys Tyr Val Leu Val Glu Leu Gln Gly Ser Asn Lys Lys Thr Ile
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aca cta atg ctg aga cga aac aat ttg tat gtg atg ggt tat tct gat	524
Thr Leu Met Leu Arg Arg Asn Asn Leu Tyr Val Met Gly Tyr Ser Asp	
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ccc ttt gaa acc aat aaa tgt cgt tac cat atc ttt aat gat atc tca	572
Pro Phe Glu Thr Asn Lys Cys Arg Tyr His Ile Phe Asn Asp Ile Ser	
105 110 115	
ggg act gaa cgc caa gat gta gag act act ctt tgc cca aat gcc aat	620
Gly Thr Glu Arg Gln Asp Val Glu Thr Leu Cys Pro Asn Ala Asn	
120 125 130	
tct cgt gtt agt aaa aac ata aac ttt gat agt cga tat cca aca ttg	668
Ser Arg Val Ser Lys Asn Ile Asn Phe Asp Ser Arg Tyr Pro Thr Leu	
135 140 145	
gaa tca aaa gcg gga gta aaa tca aga agt cag gtc caa ctg gga att	716
Glu Ser Lys Ala Gly Val Lys Ser Arg Ser Gln Val Gln Leu Gly Ile	
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Gln Ile Leu Asp Ser Asn Ile Gly Lys Ile Ser Gly Val Met Ser Phe	
165 170 175 180	
act gag aaa acc gaa gcc gaa ttc cta ttg gta gcc ata caa atg gta	812
Thr Glu Lys Thr Glu Ala Glu Phe Leu Leu Val Ala Ile Gln Met Val	
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Ser Glu Ala Ala Arg Phe Lys Tyr Ile Glu Asn Gln Val Lys Thr Asn	
200 205 210	
ttt aac aga gca ttc aac cct aat ccc aaa gta ctt aat ttg caa gag	908
Phe Asn Arg Ala Phe Asn Pro Asn Pro Lys Val Leu Asn Leu Gln Glu	
215 220 225	
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Val Leu Arg Val Asp Glu Ile Lys Pro Asp Val Ala Leu Leu Asn Tyr	
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Gln Leu Ile Met Ser Thr Tyr Tyr Asn Tyr Met Val Asn Leu Gly Asp	
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 <213> *Phytolacca americana*

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 Thr Thr Ile Ser Lys Tyr Ala Thr Phe Leu Asn Asp Leu Arg Asn Glu  
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 Ala Lys Asp Pro Ser Leu Lys Cys Tyr Gly Ile Pro Met Leu Pro Asn  
 50 55 60  
 Thr Asn Thr Asn Pro Lys Tyr Val Leu Val Glu Leu Gln Gly Ser Asn  
 65 70 75 80  
 Lys Lys Thr Ile Thr Leu Met Leu Arg Arg Asn Asn Leu Tyr Val Met  
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 Gly Tyr Ser Asp Pro Phe Glu Thr Asn Lys Cys Arg Tyr His Ile Phe  
 100 105 110  
 Asn Asp Ile Ser Gly Thr Glu Arg Gln Asp Val Glu Thr Thr Leu Cys  
 115 120 125  
 Pro Asn Ala Asn Ser Arg Val Ser Lys Asn Ile Asn Phe Asp Ser Arg  
 130 135 140  
 Tyr Pro Thr Leu Glu Ser Lys Ala Gly Val Lys Ser Arg Ser Gln Val  
 145 150 155 160  
 Gln Leu Gly Ile Gln Ile Leu Asp Ser Asn Ile Gly Lys Ile Ser Gly  
 165 170 175  
 Val Met Ser Phe Thr Glu Lys Thr Glu Ala Glu Phe Leu Leu Val Ala  
 180 185 190  
 Ile Gln Met Val Ser Glu Ala Ala Arg Phe Lys Tyr Ile Glu Asn Gln  
 195 200 205  
 Val Lys Thr Asn Phe Asn Arg Ala Phe Asn Pro Asn Pro Lys Val Leu  
 210 215 220

Asn Leu Gln Glu Thr Trp Gly Lys Ile Ser Thr Ala Ile His Asp Ala  
225 230 235 240

Lys Asn Gly Val Leu Pro Lys Pro Leu Glu Leu Val Asp Ala Ser Gly  
245 250 255

Ala Lys Trp Ile Val Leu Arg Val Asp Glu Ile Lys Pro Asp Val Ala  
260 265 270

Leu Leu Asn Tyr Val Gly Gly Ser Cys Gln Thr Thr Tyr Asn Gln Asn  
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Ala Met Phe Pro Gln Leu Ile Met Ser Thr Tyr Tyr Asn Tyr Met Val  
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Asn Leu Gly Asp Leu Phe Glu Gly Phe  
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<213> *Phytolacca americana*

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ctg atg ctt aca cca cca gct tct tca aac ata gtg ttt gac gtt gag 96  
Leu Met Leu Thr Pro Pro Ala Ser Ser Asn Ile Val Phe Asp Val Glu  
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aat gcc aca cca gaa acc tac tct aat ttt ctg act agt ttg cga gaa 144  
Asn Ala Thr Pro Glu Thr Tyr Ser Asn Phe Leu Thr Ser Leu Arg Glu  
35 40 45

gct gtg aaa gac aag aaa ttg aca tgc cat gga atg ata atg gcc aca 192  
Ala Val Lys Asp Lys Lys Leu Thr Cys His Gly Met Ile Met Ala Thr  
50 55 60

acc ctc act gaa caa ccc aag tat gtg ttg gtt gac ctc aaa ttc gga 240  
Thr Leu Thr Glu Gln Pro Lys Tyr Val Leu Val Asp Leu Lys Phe Gly  
65 70 75 80

tct gga aca ttc aca tta gca atc aga agg gga aac tta tat ttg gag 288  
Ser Gly Thr Phe Thr Leu Ala Ile Arg Arg Gly Asn Leu Tyr Leu Glu  
85 90 95

ggc tat tct gac att tac aat gga aaa tgt cgt tat cgg atc ttc aag 336  
Gly Tyr Ser Asp Ile Tyr Asn Gly Lys Cys Arg Tyr Arg Ile Phe Lys  
100 105 110

gat tca gaa tcc gat gcc caa gag acc gtt tgc ccc ggg gac aaa agc	384
Asp Ser Glu Ser Asp Ala Gln Glu Thr Val Cys Pro Gly Asp Lys Ser	
115 120 125	
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Lys Pro Gly Thr Gln Asn Asn Ile Pro Tyr Glu Lys Ser Tyr Lys Gly	
130 135 140	
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Met Glu Ser Lys Gly Gly Ala Arg Thr Lys Leu Gly Leu Gly Lys Ile	
145 150 155 160	
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Thr Leu Lys Ser Arg Met Gly Lys Ile Tyr Gly Lys Asp Ala Thr Asp	
165 170 175	
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180 185 190	
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Gln Met Val Thr Glu Ala Ser Arg Phe Lys Tyr Ile Glu Asn Lys Val	
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Lys Ala Lys Phe Asp Asp Ala Asn Gly Tyr Gln Pro Asp Pro Lys Ala	
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att tcc cta gag aaa aat tgg gac agt gtt tct aag gtc att gca aaa	720
Ile Ser Leu Glu Lys Asn Trp Asp Ser Val Ser Lys Val Ile Ala Lys	
225 230 235 240	
gtt ggc acc tcc ggt gat agt act gtt act tta cct gga gac cta aaa	768
Val Gly Thr Ser Gly Asp Ser Thr Val Thr Leu Pro Gly Asp Leu Lys	
245 250 255	
gat gag aat aat aaa cct tgg act acg gcc acc atg aac gac ctt aag	816
Asp Glu Asn Asn Lys Pro Trp Thr Thr Ala Thr Met Asn Asp Leu Lys	
260 265 270	
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Asn Asp Ile Met Ala Leu Leu Thr His Val Thr Cys Lys Val Lys Ser	
275 280 285	
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Ser Met Phe Pro Glu Ile Met Ser Tyr Tyr Tyr Arg Thr Ser Ile Ser	
290 295 300	
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Asn Leu Gly Glu Phe Glu	
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			35				40					45			
Ala	Val	Lys	Asp	Lys	Lys	Leu	Thr	Cys	His	Gly	Met	Ile	Met	Ala	Thr
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65					70					75					80
Ser	Gly	Thr	Phe	Thr	Leu	Ala	Ile	Arg	Arg	Gly	Asn	Leu	Tyr	Leu	Glu
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145					150					155					160
Thr	Leu	Lys	Ser	Arg	Met	Gly	Lys	Ile	Tyr	Gly	Lys	Asp	Ala	Thr	Asp
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Gln	Lys	Gln	Tyr	Gln	Lys	Asn	Glu	Ala	Glu	Phe	Leu	Leu	Ile	Ala	Val
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Ile	Ser	Leu	Glu	Lys	Asn	Trp	Asp	Ser	Val	Ser	Lys	Val	Ile	Ala	Lys
225					230					235					240
Val	Gly	Thr	Ser	Gly	Asp	Ser	Thr	Val	Thr	Leu	Pro	Gly	Asp	Leu	Lys
				245					250					255	
Asp	Glu	Asn	Asn	Lys	Pro	Trp	Thr	Thr	Ala	Thr	Met	Asn	Asp	Leu	Lys
				260				265					270		
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Asn Leu Gly Glu Phe Glu  
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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 12

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<210> 13

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<223> Description of Artificial Sequence: Primer

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<210> 14

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<212> DNA



<213> Artificial Sequence

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<210> 19

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<212> DNA

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<223> Description of Artificial Sequence: Primer

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ggaacatgga actttaacc tagcaagtaa cgtg

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